

What is claimed is:

1. A diverse population of labels, comprising about thirty or more unique labels, wherein each of said unique labels is bound to a nucleic acid molecule.
- 5 2. The diverse population of claim 1, wherein each of said unique labels further comprises about the same unit signal, or a multiple thereof.
3. The diverse population of claim 1, wherein each of said unique labels further comprises a mixture of
10 two or more different labels.
4. The diverse population of claim 1, further comprising unique labels having a diversity selected from a group consisting of about 40, 60, 80, 100, 120 and 140.
5. The diverse population of claim 1, further
15 comprising about 150.
6. The diverse population of claim 1, wherein said labels are fluorescent.
7. A diverse population of uniquely labeled probes, comprising about thirty or more target specific
20 nucleic acid probes each attached to a unique label bound to a nucleic acid.
8. The diverse population of claim 7, wherein each of said unique labels further comprises about the same unit signal, or a multiple thereof.

9. The diverse population of claim 7, wherein each of said unique labels further comprises a mixture of two or more different labels.

10. The diverse population of claim 7, further comprising a diversity of different labels selected from a group consisting of about 50, 100, 200, 500, 1,000, 2,000, 5,000, 1×10^4 and 3×10^4 .

11. The diverse population of claim 7, further comprising about 1×10^5 .

12. The diverse population of claim 7, wherein said labels are fluorescent.

13. The diverse population of claim 7, wherein said target specific nucleic acid further comprises said nucleic acid bound to said unique label.

14. The diverse population of claim 7, further comprising two attached populations of nucleic acids, one population of nucleic acids comprising said thirty or more target specific nucleic acid probes, and a second population of nucleic acids comprising said nucleic acid bound by a unique label.

15. The diverse population of claim 7, further comprising a nucleic acid species selected from the group consisting of a specifier, an antispecifier, a genedigit, an anti-genedigit and a dendrimer.

16. A method of producing a population of labels, comprising synthesizing a population of nucleic acids, each of said nucleic acids within said synthesized population having bound a predetermined ratio of at least
5 two different labels, wherein said population of labels has a diversity of predetermined ratios of about 30 or more.

17. The method of claim 16, wherein each of said nucleic acids bound by a predetermined ratio of at
10 least two labels further comprises about the same unit signal.

18. The method of claim 16, wherein said diversity is selected from the group consisting of 40, 60, 80, 100, 120, 140, and 150.

15 19. The method of claim 16, wherein said diversity is selected from the group consisting of 200, 500, 2,000, 5,000, 1×10^4 , 3×10^4 and 1×10^5 .

20. The method of claim 16, wherein said labels are fluorescent.

20 21. The method of claim 16, wherein each of said nucleic acids within said synthesized population further comprise an anti-genedigit.

22. The method of claim 16, wherein each of said nucleic acids within said synthesized population
25 further comprise a target specific probe.

23. A method of attaching a label to a nucleic acid probe, comprising hybridizing a nucleic acid probe having a genedigit to an anti-genedigit having a label, said genedigit comprising a set of three or more repeat
5 sequences, said anti-genedigit comprising a cognate set of at least two complimentary repeat sequences, wherein said anti-genedigit specifically hybridizes to said genedigit through a sequence having a complexity less than the number of hybridized base pairs.

10 24. The method of claim 23, wherein said nucleic acid probe further comprises a specifier.

25. The method of claim 24, wherein said specifier further comprises four or more genedigits.

15 26. The method of claim 24, wherein said specifier further comprises five or more genedigits.

27. The method of claim 23, wherein said genedigit further comprises a set of four or more repeat sequences.

20 28. The method of claim 23, wherein said anti-genedigit further comprises a cognate set of three or more complimentary repeat sequences.

29. The method of claim 23, wherein said repeat sequences or complimentary repeat sequences further comprise about 8 nucleotides.

25 30. The method of claim 23, wherein said complexity is about 8.

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31. The method of claim 23, wherein said number of hybridized base pairs is about 24.

32. The method of claim 23, further comprising hybridizing a population of nucleic acid probes having
5 different genedigits to a population of different anti-genedigits each having unique labels to produce a population of uniquely labeled nucleic acid probes.

33. The method of claim 32, wherein said nucleic acid probe further comprises a specifier.

10 34. A method of producing a population of nucleic acid probes, comprising:

(a) producing a first population of nucleic acids comprising two or more target specific probes each having at least one genedigit, said genedigit having a
15 set of three or more repeated sequences;

(b) producing a second population of nucleic acids comprising an anti-genedigit having a cognate set of at least two complimentary repeated sequences, and

(c) hybridizing said first and second
20 populations of nucleic acids to produce a population of target specific probes attached to an anti-genedigit, wherein said anti-genedigit hybridizes to said genedigit through a sequence having a complexity less than the number of hybridized base pairs.

25 35. The method of claim 34, wherein said target specific probes further comprise a specifier.

36. The method of claim 35, wherein said specifier further comprises four or more genedigits.

37. The method of claim 35, wherein said specifier further comprises five or more genedigits.

38. The method of claim 34, wherein said genedigit further comprises a set of four or more repeat
5 sequences.

39. The method of claim 34, wherein said anti-genedigit further comprises a cognate set of three complimentary repeat sequences.

40. The method of claim 34, wherein said
10 repeat sequences or complimentary repeat sequences further comprise about 8 nucleotides.

41. The method of claim 34, wherein said complexity is about 8.

42. The method of claim 34, wherein said
15 number of hybridized base pairs is about 24.

43. The method of claim 34, wherein said two or more target specific probes further comprise at least one different genedigit.

44. The method of claim 34, wherein said
20 population of anti-genedigits further comprises two or more different anti-genedigits.

45. The method of claim 34, wherein said anti-genedigit further comprises a label.

46. The method of claim 44, wherein said two or more different anti-genedigits further comprise unique labels.

47. The method of claim 34, further comprising
5 hybridizing a population of target specific probes having different genedigits to a population of different anti-genedigits each having a unique label to produce a population of uniquely labeled nucleic acid probes.

48. The method of claim 47, wherein said
10 target specific nucleic acid probe further comprises a specifier.

49. A method of producing a population of uniquely labeled nucleic acid probes, comprising:
15 (a) synthesizing a population of target specific nucleic acid probes each having a different specifier;
(b) synthesizing a corresponding population of anti-genedigits each having a unique label, said
20 population having a diversity sufficient to uniquely hybridize to genedigits within said specifiers, and
(c) hybridizing said populations of target nucleic acid probes to said anti-genedigits, to produce a population wherein each of said target specific probes is
25 uniquely labeled.

50. A method of detecting a nucleic acid analyte, comprising:

(a) contacting a mixture of nucleic acid analytes with a plurality of target specific probes each
30 attached to a unique label bound to a nucleic acid under

conditions sufficient for hybridization of said probes to said target, and

(b) measuring a signal from one or more said target specific probes hybridized to an analyte, wherein
5 said signal uniquely identifies the analyte species.

51. The method of claim 50, wherein each of said unique labels further comprises about the same unit signal, or multiple thereof.

52. The method of claim 50, wherein each of
10 said unique labels further comprises a mixture of two or more different labels.

53. The method of claim 50, wherein said plurality of target specific probes further comprises different target specific probes selected from the group
15 consisting of about 50, 100, 200, 500, 1,000, 2,000, 5,000, 1×10^4 , 3×10^4 and 1×10^5 .

54. The method of claim 50, wherein said plurality of target specific probes further comprises at least one target specific probe for each nucleic acid
20 analyte in said mixture.

55. The method of claim 50, wherein said mixture further comprises an expressed RNA population or DNA copy thereof.

56. The method of claim 50, wherein said
25 labels are fluorescent.

57. The method of claim 50, wherein said target specific nucleic acid further comprises said nucleic acid bound to said unique label.

58. The diverse population of claim 50,
5 further comprising two attached populations of nucleic
acids, one population of nucleic acids comprising said
plurality of target specific nucleic acid probes, and a
second population of nucleic acids comprising said
nucleic acid bound by a unique label.

10 59. The diverse population of claim 50,
further comprising a nucleic acid species selected from
the group consisting of a specifier, an antispecifier, a
genedigit, an anti-genedigit and a dendrimer.

60. The method of claim 50, further comprising
15 detecting a single copy of an analyte within said
mixture.

61. A method of detecting a nucleic acid analyte, comprising:

(a) contacting a mixture of nucleic acid
20 analytes under conditions sufficient for hybridization
with a target specific probe having at least one
genedigit, said genedigit having a set of three or more
repeated sequences;

(b) contacting said mixture under conditions
25 sufficient for hybridization with an anti-genedigit
having a cognate set of at least two complimentary
repeated sequences, and

(c) detecting a hybridized complex comprising said analyte, target specific probe and said anti-

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genedigit, wherein said anti-genedigit hybridizes to said genedigit through a sequence having a complexity less than the number of hybridized base pairs.

62. The method of claim 61, wherein said
5 target specific probe further comprises a specifier.

63. The method of claim 62, wherein said specifier further comprises four or more genedigits.

64. The method of claim 62, wherein said specifier further comprises five or more genedigits.

10 65. The method of claim 61, wherein said genedigit further comprises a set of four or more repeat sequences.

66. The method of claim 61, wherein said anti-genedigit further comprises a cognate set of three
15 complimentary repeat sequences.

67. The method of claim 61, wherein said repeat sequences or complimentary repeat sequences further comprise about 8 nucleotides.

68. The method of claim 61, wherein said
20 complexity is about 8.

69. The method of claim 61, wherein said number of hybridized base pairs is about 24.

70. The method of claim 61, further comprising two or more target specific probes

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71. The method of claim 70, further comprising at least one different genedigit.

72. The method of claim 70, further comprising two or more different anti-genedigits.

5 73. The method of claim 61, wherein said anti-genedigit further comprises a label.

74. The method of claim 72, wherein said two or more different anti-genedigits further comprise unique labels.

10 75. The method of claim 61, further comprising a plurality of target specific probes having different genedigits and a plurality of different anti-genedigits each having a unique label.

15 76. The method of claim 75, wherein said target specific probes further comprise a specifier.

77. A method of detecting a nucleic acid analyte, comprising:

20 (a) contacting a mixture of nucleic acid analytes under conditions sufficient for hybridization with a plurality of target specific nucleic acid probes each having a different specifier;

25 (b) contacting said mixture under conditions sufficient for hybridization with a corresponding plurality of anti-genedigits each having a unique label, said plurality of anti-genedigits having a diversity sufficient to uniquely hybridize to genedigits within said specifiers, and

(c) uniquely detecting a hybridized complex between one or more analytes in said mixture, a target specific probe, and an anti-genedigit.

78. A nucleic acid labeling kit, comprising a
5 set of genedigits, a set of anti-genedigits and a unique
set of labels bound to a nucleic acid.

79. The kit of claim 78, further comprising a specifier.

80. The kit of claim 78, further comprising a
10 dendrimer.

81. The kit of claim 78, wherein said unique label further comprises a ratio of two different labels.

82. The kit of claim 78, wherein said unique label is fluorescent.

15 83. The kit of claim 78, further comprising a
diverse population of unique labels.

84. The kit of claim 83, wherein said diversity is selected from the group consisting of 50, 100, 150, 200, 500, 1,000, 2,000, 5,000, 1×10^4 , 3×10^4 and 1×10^5 .